OIPE

RAW SEQUENCE LISTING   DATE: 12/11/2001
PATENT APPLICATION: US/10/001,863   TIME: 12:10:36

Input Set : A:\isph-618sequence.txt
Output Set: N:\CRF3\12112001\I001863.raw   **ENTERED**

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 5 <110> APPLICANT: James Karras
 6        Erich Koller
 8 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF TOLL-LIKE RECEPTOR 4 EXPRESSION
10 <130> FILE REFERENCE: ISPH-0618
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/001,863
C--> 12 <141> CURRENT FILING DATE: 2001-11-19
12 <160> NUMBER OF SEQ ID NOS: 33
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 20
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Antisense Oligonucleotide
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25 tccgtcatcg ctcctcaggg                                    20
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28 <211> LENGTH: 20
29 <212> TYPE: DNA
30 <213> ORGANISM: Artificial Sequence
32 <220> FEATURE:
33 <223> OTHER INFORMATION: Antisense Oligonucleotide
35 <400> SEQUENCE: 2
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40 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
43 <220> FEATURE:
45 <221> NAME/KEY: CDS
46 <222> LOCATION:, (285)...(2684)
48 <400> SEQUENCE: 3
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50 gcctggctgg gactctgatc ccagccatgg ccttcctctc ctgcgtgaga ccagaaagct 120
51 gggagccctg cgtggagact tggccctaaa ccacacagaa gagctggcat gaaacccaga 180
52 gctttcagac tccggagcct cagcccttca ccccgattcc attgcttctt gctaaatgct 240
53 gccgttttat cacggaggtg gttcctaata ttacttatca atgc atg gag ctg aat 296
54                                                  Met Glu Leu Asn
55                                                   1
57 ttc tac aaa atc ccc gac aac ctc ccc ttc tca acc aag aac ctg gac 344
58 Phe Tyr Lys Ile Pro Asp Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp
59  5                  10                  15                  20
61 ctg agc ttt aat ccc ctg agg cat tta ggc agc tat agc ttc ttc agt 392
62 Leu Ser Phe Asn Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Phe Ser
63                 25                  30                  35
65 ttc cca gaa ctg cag gtg ctg gat tta tcc agg tgt gaa atc cag aca 440
66 Phe Pro Glu Leu Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr
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67                40              45                50
69 att gaa gat ggg gca tat cag agc cta agc cac ctc tct acc tta ata    488
70 Ile Glu Asp Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile
71         55              60                65
73 ttg aca gga aac ccc atc cag agt tta gcc ctg gga gcc ttt tct gga    536
74 Leu Thr Gly Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly
75       70              75              80
77 cta tca agt tta cag aag ctg gtg gct gtg gag aca aat cta gca tct    584
78 Leu Ser Ser Leu Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser
79 85              90                95                100
81 cta gag aac ttc ccc att gga cat ctc aaa act ttg aaa gaa ctt aat    632
82 Leu Glu Asn Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn
83             105             110               115
85 gtg gct cac aat ctt atc caa tct ttc aaa tta cct gag tat ttt tct    680
86 Val Ala His Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser
87             120             125             130
89 aat ctg acc aat cta gag cac ttg gac ctt tcc agc aac aag att caa    728
90 Asn Leu Thr Asn Leu Glu His Leu Asp Leu Ser Ser Asn Lys Ile Gln
91         135             140             145
93 agt att tat tgc aca gac ttg cgg gtt cta cat caa atg ccc cta ctc    776
94 Ser Ile Tyr Cys Thr Asp Leu Arg Val Leu His Gln Met Pro Leu Leu
95      150             155             160
97 aat ctc tct tta gac ctg tcc ctg aac cct atg aac ttt atc caa cca    824
98 Asn Leu Ser Leu Asp Leu Ser Leu Asn Pro Met Asn Phe Ile Gln Pro
99 165             170             175             180
101 ggt gca ttt aaa gaa att agg ctt cat aag ctg act tta aga aat aat   872
102 Gly Ala Phe Lys Glu Ile Arg Leu His Lys Leu Thr Leu Arg Asn Asn
103             185             190               195
105 ttt gat agt tta aat gta atg aaa act tgt att caa ggt ctg gct ggt   920
106 Phe Asp Ser Leu Asn Val Met Lys Thr Cys Ile Gln Gly Leu Ala Gly
107             200             205             210
109 tta gaa gtc cat cgt ttg gtt ctg gga gaa ttt aga aat gaa gga aac   968
110 Leu Glu Val His Arg Leu Val Leu Gly Glu Phe Arg Asn Glu Gly Asn
111             215             220             225
113 ttg gaa aag ttt gac aaa tct gct cta gag ggc ctg tgc aat ttg acc   1016
114 Leu Glu Lys Phe Asp Lys Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr
115       230             235             240
117 att gaa gaa ttc cga tta gca tac tta gac tac tac ctc gat gat att   1064
118 Ile Glu Glu Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr Leu Asp Asp Ile
119 245             250             255             260
121 att gac tta ttt aat tgt ttg aca aat gtt tct tca ttt tcc ctg gtg   1112
122 Ile Asp Leu Phe Asn Cys Leu Thr Asn Val Ser Ser Phe Ser Leu Val
123             265             270             275
125 agt gtg act att gaa agg gta aaa gac ttt tct tat aat ttc gga tgg   1160
126 Ser Val Thr Ile Glu Arg Val Lys Asp Phe Ser Tyr Asn Phe Gly Trp
127             280             285             290
129 caa cat tta gaa tta gtt aac tgt aaa ttt gga cag ttt ccc aca ttg   1208
130 Gln His Leu Glu Leu Val Asn Cys Lys Phe Gly Gln Phe Pro Thr Leu
131         295             300             305
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133 aaa ctc aaa tct ctc aaa agg ctt act ttc act tcc aac aaa ggt ggg   1256
134 Lys Leu Lys Ser Leu Lys Arg Leu Thr Phe Thr Ser Asn Lys Gly Gly
135     310                 315                 320
137 aat gct ttt tca gaa gtt gat cta cca agc ctt gag ttt cta gat ctc   1304
138 Asn Ala Phe Ser Glu Val Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu
139 325                 330                 335                 340
141 agt aga aat ggc ttg agt ttc aaa ggt tgc tgt tct caa agt gat ttt   1352
142 Ser Arg Asn Gly Leu Ser Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe
143                 345                 350                 355
145 ggg aca acc agc cta aag tat tta gat ctg agc ttc aat ggt gtt att   1400
146 Gly Thr Thr Ser Leu Lys Tyr Leu Asp Leu Ser Phe Asn Gly Val Ile
147                 360                 365                 370
149 acc atg agt tca aac ttc ttg ggc tta gaa caa cta gaa cat ctg gat   1448
150 Thr Met Ser Ser Asn Phe Leu Gly Leu Glu Gln Leu Glu His Leu Asp
151         375                 380                 385
153 ttc cag cat tcc aat ttg aaa caa atg agt gag ttt tca gta ttc cta   1496
154 Phe Gln His Ser Asn Leu Lys Gln Met Ser Glu Phe Ser Val Phe Leu
155         390                 395                 400
157 tca ctc aga aac ctc att tac ctt gac att tct cat act cac acc aga   1544
158 Ser Leu Arg Asn Leu Ile Tyr Leu Asp Ile Ser His Thr His Thr Arg
159 405                 410                 415                 420
161 gtt gct ttc aat ggc atc ttc aat ggc ttg tcc agt ctc gaa gtc ttg   1592
162 Val Ala Phe Asn Gly Ile Phe Asn Gly Leu Ser Ser Leu Glu Val Leu
163                 425                 430                 435
165 aaa atg gct ggc aat tct ttc cag gaa aac ttc ctt cca gat atc ttc   1640
166 Lys Met Ala Gly Asn Ser Phe Gln Glu Asn Phe Leu Pro Asp Ile Phe
167                 440                 445                 450
169 aca gag ctg aga aac ttg acc ttc ctg gac ctc tct cag tgt caa ctg   1688
170 Thr Glu Leu Arg Asn Leu Thr Phe Leu Asp Leu Ser Gln Cys Gln Leu
171             455                 460                 465
173 gag cag ttg tct cca aca gca ttt aac tca ctc tcc agt ctt cag gta   1736
174 Glu Gln Leu Ser Pro Thr Ala Phe Asn Ser Leu Ser Ser Leu Gln Val
175     470                 475                 480
177 cta aat atg agc cac aac aac ttc ttt tca ttg gat acg ttt cct tat   1784
178 Leu Asn Met Ser His Asn Asn Phe Phe Ser Leu Asp Thr Phe Pro Tyr
179 485                 490                 495                 500
181 aag tgt ctg aac tcc ctc cag gtt ctt gat tac agt ctc aat cac ata   1832
182 Lys Cys Leu Asn Ser Leu Gln Val Leu Asp Tyr Ser Leu Asn His Ile
183                 505                 510                 515
185 atg act tcc aaa aaa cag gaa cta cag cat ttt cca agt agt cta gct   1880
186 Met Thr Ser Lys Lys Gln Glu Leu Gln His Phe Pro Ser Ser Leu Ala
187                 520                 525                 530
189 ttc tta aat ctt act cag aat gac ttt gct tgt act tgt gaa cac cag   1928
190 Phe Leu Asn Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Gln
191             535                 540                 545
193 agt ttc ctg caa tgg atc aag gac cag agg cag ctc ttg gtg gaa gtt   1976
194 Ser Phe Leu Gln Trp Ile Lys Asp Gln Arg Gln Leu Leu Val Glu Val
195     550                 555                 560
197 gaa cga atg gaa tgt gca aca cct tca gat aag cag ggc atg cct gtg   2024
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198 Glu Arg Met Glu Cys Ala Thr Pro Ser Asp Lys Gln Gly Met Pro Val
199 565                 570                 575                 580
201 ctg agt ttg aat atc acc tgt cag atg aat aag acc atc att ggt gtg  2072
202 Leu Ser Leu Asn Ile Thr Cys Gln Met Asn Lys Thr Ile Ile Gly Val
203                 585                 590                 595
205 tcg gtc ctc agt gtg ctt gta gta tct gtt gta gca gtt ctg gtc tat  2120
206 Ser Val Leu Ser Val Leu Val Val Ser Val Val Ala Val Leu Val Tyr
207                 600                 605                 610
209 aag ttc tat ttt cac ctg atg ctt ctt gct ggc tgc ata aag tat ggt  2168
210 Lys Phe Tyr Phe His Leu Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly
211             615                 620                 625
213 aga ggt gaa aac atc tat gat gcc ttt gtt atc tac tca agc cag gat  2216
214 Arg Gly Glu Asn Ile Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp
215         630                 635                 640
217 gag gac tgg gta agg aat gag cta gta aag aat tta gaa gaa ggg gtg  2264
218 Glu Asp Trp Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val
219 645                 650                 655                 660
221 cct cca ttt cag ctc tgc ctt cac tac aga gac ttt att ccc ggt gtg  2312
222 Pro Pro Phe Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val
223                 665                 670                 675
225 gcc att gct gcc aac atc atc cat gaa ggt ttc cat aaa agc cga aag  2360
226 Ala Ile Ala Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys
227                 680                 685                 690
229 gtg att gtt gtg gtg tcc cag cac ttc atc cag agc cgc tgg tgt atc  2408
230 Val Ile Val Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile
231             695                 700                 705
233 ttt gaa tat gag att gct cag acc tgg cag ttt ctg agc agt cgt gct  2456
234 Phe Glu Tyr Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala
235         710                 715                 720
237 ggt atc atc ttc att gtc ctg cag aag gtg gag aag acc ctg ctc agg  2504
238 Gly Ile Ile Phe Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg
239 725                 730                 735                 740
241 cag cag gtg gag ctg tac cgc ctt ctc agc agg aac act tac ctg gag  2552
242 Gln Gln Val Glu Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu
243                 745                 750                 755
245 tgg gag gac agt gtc ctg ggg cgg cac atc ttc tgg aga cga ctc aga  2600
246 Trp Glu Asp Ser Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg
247                 760                 765                 770
249 aaa gcc ctg ctg gat ggt aaa tca tgg aat cca gaa gga aca gtg ggt  2648
250 Lys Ala Leu Leu Asp Gly Lys Ser Trp Asn Pro Glu Gly Thr Val Gly
251             775                 780                 785
253 aca gga tgc aat tgg cag gaa gca aca tct atc tga agaggaaaaa        2694
254 Thr Gly Cys Asn Trp Gln Glu Ala Thr Ser Ile
255         790                 795
257 taaaaacctc ctgaggcatt tcttgcccag ctgggtccaa cacttgttca gttaataagt 2754
258 attaaatgct gccacatgtc aggccttatg ctaagggtga gtaattccat ggtgcactag 2814
259 atatgcaggg ctgctaatct caaggagctt ccagtgcaga gggaataaat gctagactaa 2874
260 aatacagagt cttccaggtg ggcatttcaa ccaactcagt caaggaaccc atgacaaaga 2934
261 aagtcatttc aactcttacc tcatcaagtt gaataaagac agagaaaaca gaaagagaca 2994
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262 ttgttctttt cctgagtctt ttgaatggaa attgtattat gttatagcca tcataaaacc 3054
263 attttggtag ttttgactga actgggtgtt cactttttcc tttttgattg aatacaattt 3114
264 aaattctact tgatgactgc agtcgtcaag gggctcctga tgcaagatgc cccttccatt 3174
265 ttaagtctgt ctccttacag aggttaaagt ctaatggcta attcctaagg aaacctgatt 3234
266 aacacatgct cacaaccatc ctggtcattc tcgaacatgt tctatttttt aactaatcac 3294
267 ccctgatata tttttatttt tatatatcca gttttcattt ttttacgtct tgcctataag 3354
268 ctaatatcat aaataaggtt gtttaagacg tgcttcaaat atccatatta accactattt 3414
269 ttcaaggaag tatggaaaag tacactctgt cactttgtca ctcgatgtca ttccaaagtt 3474
270 attgcctact aagtaatgac tgtcatgaaa gcagcattga aataatttgt ttaaaggggg 3534
271 cactcttta aacgggaaga aaatttccgc ttcctggtct tatcatggac aatttgggct 3594
272 ataggcatga aggaagtggg attacctcag gaagtcacct tttcttgatt ccagaaacat 3654
273 atgggctgat aaacccgggg tgacctcatg aaatgagttg cagcagatgt ttattttttt 3714
274 cagaacaagt gatgtttgat ggacctatga atctatttag ggagacacag atggctggga 3774
275 tccctcccct gtaccttct cactgacagg agaacta                           3811
277 <210> SEQ ID NO: 4
278 <211> LENGTH: 20
279 <212> TYPE: DNA
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283 <223> OTHER INFORMATION: Antisense Oligonucleotide
285 <400> SEQUENCE: 4
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289 <211> LENGTH: 20
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291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Antisense Oligonucleotide
296 <400> SEQUENCE: 5
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300 <211> LENGTH: 20
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <223> OTHER INFORMATION: Antisense Oligonucleotide
307 <400> SEQUENCE: 6
308 agggccaagt ctccacgcag                                            20
310 <210> SEQ ID NO: 7
311 <211> LENGTH: 20
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial Sequence
315 <220> FEATURE:
316 <223> OTHER INFORMATION: Antisense Oligonucleotide
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321 <210> SEQ ID NO: 8
322 <211> LENGTH: 20
323 <212> TYPE: DNA
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date